

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Sutcliffe, Gregor J., et al. )  
Division of ) Prior Art Unit: 1653  
Serial No.: 09/230,896 )  
Filed: December 12, 2000 ) Prior Examiner: Stephen Tu  
(By Express Mail) )  
For: HYPOTHALAMUS-SPECIFIC ) Atty. Docket No. TSRI 548.1 DIV. 1  
POLYPEPTIDES )

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09/735138  
12/12/00

STATEMENT UNDER 37 CFR 1.825

Commissioner for Patents  
BOX PATENT APPLICATION  
Washington, D. C. 20231

Sir:

I hereby state that, to the best of my information and belief, the content of the paper and computer readable copies of the substitute sequence listing submitted pursuant to 37 CFR 1.825, respectively, is the same.

Respectfully submitted,

OLSON & HIERL, LTD.

By Talivaldis Cepuritis  
Talivaldis Cepuritis (Reg. No. 20,818)

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SCANNED, #

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Sutcliffe, J. Gregor  
Gautvik, Kaare M.  
De Lecea, Luis  
Bloom, Floyd E.  
Danielson, Patria E.  
Kilduff, T.S.  
Gautvik, Vigdis T.  
Foye, Pamela E.

(ii) TITLE OF INVENTION: Hypothalamus-Specific Polypeptides

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Olson & Hierl, Ltd.  
(B) STREET: 20 North Wacker Drive, 36th Floor  
(C) CITY: Chicago  
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(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not yet Known (Division of 09/230,896  
filed 02-FEB-1999)  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/023,220  
(B) FILING DATE: 02-AUG-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Talivaldis Cepuritis  
(B) REGISTRATION NUMBER: 20,818  
(C) REFERENCE/DOCKET NUMBER: TSRI 548.1 DIV.1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-580-1180  
(B) TELEFAX: 312-580-1189

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Asn Leu Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
1           5           10           15
Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
20           25           30
Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
35           40           45
Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
50           55           60
Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
65           70           75           80
Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
85           90           95
Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr Pro Cys Pro Gly Arg
100          105          110
Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala Pro Arg Gly Gly Ser
115          120          125

Arg Val
130

```

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Asn Phe Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
1           5           10           15
Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
20           25           30

```

Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu  
 35 40 45  
 Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr  
 50 55 60  
 Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln  
 65 70 75 80  
 Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met  
 85 90 95  
 Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro His Pro Cys Ser Gly Arg  
 100 105 110  
 Gly Cys Pro Thr Val Thr Thr Thr Ala Leu Ala Pro Arg Gly Gly Ser  
 115 120 125  
 Gly Val  
 130

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 569 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAAGACGACG GCCTCAGACT CCTTGGGTAT TTGGACCACT GCACCGAAGA TACCATCTCT	60
CCGGATTACC TCTCCCTGAG CTCCAGACAC CATGAACCTT CCTTCTACAA AGGTTCCTTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCGCCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCGCAG CCTCTGCCCC ACTGCTGTCTG CCAGAAGACG TGTTCCTGCC GGCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCCGC GGGCATCCTC ACTCTGGGAA AGCGGCGACC	300
TGGACCCCCA GGCCTCCAAG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAT ATCCCTGCCC	420
TGCTCGCCGC TGTCCGACTG CAACCGCCAC CGCTTTAGCG CCCCAGGGCG GATCCAGAGT	480
CTGAACCCGT CTTCTATCCC TGTCCTAGTC CTAACCTTCC CCTCTCCTCG CCAGTCCCTA	540
GGCAATAAAG ACGTTTCTCT GTTGGTGTG	569

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAAGACGACG GCCTCAGACT TCTTGGGTAT TTGGACCACT GCACTGAAGA GATCATCTCT	60
CCAGATTACT TTCCCCTGAG CTCCAGGCAC CATGAACTTT CCTTCTACAA AGGTTCCCTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCACCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCACAG CCTCTGCCCC ACTGCTGTCG CCAGAAGACG TGTTCCTGCC GTCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCTGC GGGTATCCTG ACTCTGGGAA AGCGGCGGCC	300
TGGACCTCCA GGCCTCCAGG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAC ATCCCTGCTC	420
TGGTCGCGGC TGTCCGACCG TAACTATCAC CGCTTTAGCA CCCCGGGGAG GGTCCGGAGT	480
TTGAACCCAT CTTCTATCCT TGTCCTGATC CAACTTCCC CCTCTGCTCG CCGCTGTCAG	540
TCTCTTGGTA AATGGCAATA AAGACGTTTC TCTGTTGGTG TG	582

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1458 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTAGGAGAC ATTGCGGCGG CGGTGGCGGC GTTGGCAGCA GCTGCAGACA TGCTGCTGCT	60
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CAAGAAACAG ACGGAGGACA TCAGCAGTGT CTATGAGATC CGGGAGAAGC TGGGCTCGGG	120
TGCCTTCTCT GAGGTGATGC TGGCCCAGGA AAGGGGCTCT GCTCATCTTG TGGCCCTCAA	180
GTGCATTCCC AAGAAAGCAC TTCGGGGCAA GGAGGCCCTG GTGGAGAATG AGATCGCAGT	240
ACTCCGCAGG ATTAGCCACC CCAACATTGT GGCTCTGGAG GACGTCCACG AGAGCCCTTC	300
CCATCTCTAC TTGGCCATGG AGCTGGTAAC AGGTGGTGAA CTGTTTGACC GAATCATGGA	360
GCGGGGCTCC TACACAGAGA AGGATGCGAG CCACCTTGTA GGGCAGGTCC TTGGTGCTGT	420
CTCCTACCTT CATAGCCTGG GCATCGTGCA CCGGGACCTC AAGCCTGAAA ACCTCCTCTA	480
TGCCACACCT TTTGAGGACT CCAAGATCAT GGTCTCTGAC TTTGGCCTGT CCAAATTCA	540
AGCTGGCAAC ATGCTAGGCA CAGCCTGTGG GACCCAGGA TATGTGGCCC CAGAGCTCCT	600
GGAGCAGAAA CCCTACGGGA AGGCCGTAGA TGTGTGGGCC CTGGGTGTCA TCTCCTACAT	660
CCTGCTGTGT GGGTACCCCC CTTCTATGA TGAGAGCGAT CCTGAACTCT TCAGCCAGAT	720
TCTGAGGGCC AGCTACGAGT TTGACTCTCC CTTTGGGGAT GACATCTCAG AATCAGCCAA	780
AGACTTCATT CGGCACCTTC TGGAACGTGA TCCCCAGAAG AGGTTACCT GCCAACAGGC	840
CTTACAGCAT CTCTGGATCT CTGGGGATGC AGCCTTGGAC AGGGACATCC TAGGTTCTGT	900
CAGTGAGCAG ATCCAGAAGA ATTTTGCCAG GACCCACTGG AAGCGTGCAT TCAATGCCAC	960
ATCATTCCTA CGTCACATCC GTAAGCTGGG ACAGAGCCCA GAGGGTGAGG AGGCCTCCAG	1020
GCAGGGTATG ACCCGTCACA GCCACCCAGG CCTTGGGACT AGCCAGTCTC CCAAGTGGTG	1080
ACAACCAGGT GGATGCCAAG GAAGGCCAAG TGGACTGACT CCTAGCTTTT CTTTCCTCCA	1140
GCCCTTTTGA TCTCCTTCCC TGATCCTTGT CCCCCGACT GGCCTCTGTT GGAAAGTCCA	1200
AGACCGTGGG TGTGATGCAT GGCCTGGGG TATGGGGCTT CCCAAGTATG TCCCCAGCCT	1260
CTGTCCTTTG TTGCTGCCAC CCTCTATGGA AACTGAGGAG GTATTCAAAA ATGGATTGG	1320
GGGCCATCCT TCCTGCACCT TGCACGCACA TATGCATTGC GTGGCTGTTC TGTGCTTTGC	1380
TGACTGTGGG TGGTCCTGCT TGTGTTGTAG CCCTTTAGTT CCTCCTCTTT CCAACCAATA	1440
AAGACAAACA GAACAATG	1458

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
1           5           10           15
Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
20           25           30
Ala Gly Ile Leu Thr Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu
35           40           45
Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala
50           55           60
Gly Ile Leu Thr Met Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr
65           70           75           80
Pro Cys Pro Gly Arg Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala
85           90           95
Pro Arg Gly Gly Ser Arg Val
100
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
1           5           10           15
Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
20           25           30
Ala Gly Ile Leu Thr Leu Gly
35
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu	Gly	Val	Asp	Ala	Gln	Pro	Leu	Pro	Asp	Cys	Cys	Arg	Gln	Lys	Thr
1				5					10					15	
Cys	Ser	Cys	Arg	Leu	Tyr	Glu	Leu	Leu	His	Gly	Ala	Gly	Asn	His	Ala
			20					25					30		
Ala	Gly	Ile	Leu	Thr	Leu										
		35													

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala
1				5				10						15	
Asn	Gly	Asn	His	Ala	Ala	Gly	Ile	Leu	Thr	Met	Gly				
			20					25							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:



Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala  
1 5 10 15  
Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met  
20 25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile  
1 5 10 15  
Leu Thr Leu Gly  
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile  
1 5 10 15  
Leu Thr Met Gly  
20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Asn His Ala Ala Gly Ile Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAACCTTC CTTCTACAAA GGTTCCCTGG GCCGCCGTGA CGCTGCTGCT GCTGCTACTG	60
CTGCCGCCGG CGCTGCTGTC GCTTGGGGTG GACGCGCAGC CTCTGCCCCGA CTGCTGTCGC	120
CAGAAGACGT GTTCCTGCCG TCTCTACGAA CTGTTGCACG GAGCTGGCAA CCACGCCGCG	180
GGCATCCTCA CTCTGGGAAA GCGGCGACCT GGACCCCCAG GCCTCCAAGG ACGGCTGCAG	240
CGCCTCCTTC AGGCCAACGG TAACCACGCA GCTGGCATCC TGACCATGGG CCGCCGCGCA	300
GGCGCAGAGC TAGAGCCATA TCCCTGCCCT GGTCGCCGCT GTCCGACTGC AACCGCCACC	360
GCTTTAGCGC CCCGGGGCGG ATCCAGAGTC TGA	393

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAACTTTC	CTTCTACAAA	GGTTCCTG	GCCGCCGTGA	CGCTGCTGCT	GCTGCTACTG	60
CTGCCGCCGG	CGCTGCTGTC	GCTTGGGGTG	GACGCACAGC	CTCTGCCCCG	CTGCTGTCGC	120
CAGAAGACGT	GTTCTTGCCG	TCTCTACGAA	CTGTTGCACG	GAGCTGGCAA	CCACGCTGCG	180
GGTATCCTGA	CTCTGGGAAA	GCGGCGGCCT	GGACCTCCAG	GCCTCCAGGG	ACGGCTGCAG	240
CGCTTCCTTC	AGGCCAACGG	TAACCACGCA	GCTGGCATCC	TGACCATGGG	CCGCCGCGCA	300
GGCGCAGAGC	TAGAGCCACA	TCCCTGCTCT	GGTCGCGGCT	GTCCGACCGT	AACTACCACC	360
GCTTTAGCAC	CCCGGGGAGG	GTCCGGAGTC	TGA			393

[illegible]